

First, load packages.

```
RLang> library(matR)
RLang> library(vegan)
```

Make a collection.

```
RLang> IDs <- matR:::scrubIds(c('4441679.3 4441680.3 4441682.3 4441695.3 4441696.3 4440463.3 4440464.3'),
RLang> names(IDs) <- c('cow rumen (a)', 'cow rumen (b)', 'cow rumen (c)', 'fish gut (a)', 'fish gut (b)', 'le
RLang> cc <- collection(IDs)
```

Vegan package produces a rarefaction curve.

```
RLang> m <- t(cc$raw)
RLang> rownames(m) <- names(cc)
RLang> rarecurve(m, step=20, cex = 0.8, xlab='sample size', ylab='species')
RLang> title("rarefaction")
```

